



SEQUENCE LISTING

<110> Krolewski, Andrzej S.
Pezzolesi, Marcus G.
Nagase, Terumasa

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<151> 2002-10-28

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Asp Ser Asp Leu Arg Gly Pro Ser Leu Arg Ser Gln Ser Gln Glu Leu		380
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Pro Glu Met Asp Ser Phe Ser Ser Glu Asp Pro Arg Asp Thr Glu Thr		395
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Ser Thr Ser Ala Ser Thr Ser Asp Val Gly Phe Leu Pro Leu Thr Phe		415
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Gly Pro His Ala Ser Ile Glu Glu Glu Ala Arg Glu Asp Pro Leu Pro		430
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Pro Gly Leu Leu Pro Glu Met Ala His Leu Ser Gly Gly Pro Phe Ala		445
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Glu Gln Pro Gly Trp Arg Asn Leu Gly Gly Glu Ser Pro Ser Leu Pro		460
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Gln Gly Ser Leu Phe His Ser Gly Thr Ala Ser Ser Ser Gln Asn Gly		475
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His Glu Glu Gly Ala Thr Gly Asp Arg Glu Asp Gly Pro Gly Val Ala		495
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<220>

<223> Exemplary motif

<221> VARIANT

<222> 2-8, 10-15, 17-22, 24-31

<223> Xaa = Any Amino Acid

<400> 7

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<213> Homo sapiens

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<211> 401

<212> DNA

<213> Homo sapiens

<400> 15

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<211> 401

<212> DNA

<213> Homo sapiens

<400> 16

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<211> 401

<212> DNA

<213> Homo sapiens

<400> 17

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<211> 401

<212> DNA

<213> Homo sapiens

<400> 18

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<211> 416

<212> DNA

<213> Homo sapiens

<400> 19

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<211> 400

<212> DNA

<213> Homo sapiens

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<210> 21

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<212> DNA

<213> Homo sapiens

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<211> 401

<212> DNA

<213> Homo sapiens

<400> 22

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<211> 401

<212> DNA

<213> Homo sapiens

<400> 27

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<211> 401

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

<400> 29

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<213> Homo sapiens

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gccagcctgg	gcactggagc	tggaaggggc	ttcccgggcc	cctccctctg	caccttccca	240
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gagaaggaca	attgctaagc	agttcctccc	gatgcaaagc	tcaaaacaag	ccccagggtcc	360

tcctgctcag tgtgagagag aggacgacga aggagggaaa c 401

<210> 31

<211> 401

<212> DNA

<213> Homo sapiens

<400> 31

ccaaggtgtg	gctggaggaa	gcagagtcta	ctcccgctaa	gtctgtccgc	tcactgctgg	60
ccaaagctgc	cctgcgtctc	ctccccaccg	ccagccagag	ggaacctgca	atttcacctc	120
atntagaggt	aaaacatcta	aatttaacgt	tatgggcttt	tggggctggg	tggcttttat	180
gcctgagtc	ctcacttagg	gtcctttttt	atccactcaa	atgccagcta	gggcttagtt	240
tgtttatagg	agtttccaaa	atagctcctt	tggtttcgca	tgaaaggaaa	tggcaaaata	300
gccaggaag	aggaatgtga	gtttacacag	aagacagaca	ggcgcccgag	gaggcttctc	360
tgggaaccag	ttcgctgta	ccagaggggg	cccgagaaag	t		401

<210> 32

<211> 401

<212> DNA

<213> Homo sapiens

<400> 32

ccaaggtgtg	gctggaggaa	gcagagtcta	ctcccgctaa	gtctgtccgc	tcactgctgg	60
ccaaagctgc	cctgcgtctc	ctccccaccg	ccagccagag	ggaacctgca	atttcacctc	120
atntagaggt	aaaacatcta	aatttaacgt	tatgggcttt	tggggctggg	tggcttttat	180
gcctgagtc	ctcacttagg	actccttttt	atccactcaa	atgccagcta	gggcttagtt	240
tgtttatagg	agtttccaaa	atagctcctt	tggtttcgca	tgaaaggaaa	tggcaaaata	300
gccaggaag	aggaatgtga	gtttacacag	aagacagaca	ggcgcccgag	gaggcttctc	360
tgggaaccag	ttcgctgta	ccagaggggg	cccgagaaag	t		401

<210> 33

<211> 401

<212> DNA

<213> Homo sapiens

<400> 33

tacgttagaa	ggaccctacg	ttagaaggg	gaggcgctag	ggccatagcc	taagggcact	60
gggaaccctg	tgggcatg	cagttcaagc	ccatccccgc	tccctccagc	tgtgtccat	120
cctgccaca	cctgaccatt	tgcctaacct	agatccttcc	tgtcttgcat	ttcctcaagc	180
atccggagcc	caggactgct	gagtcaacct	tctggaatgc	ccacaactcc	ccacaggcca	240
gccggccttg	ggactccgc	acagccacgt	gagccgggtg	agccgggtct	gtttgctagt	300
ggaggctgtt	aacagcacgg	gaagtggta	agggttcaac	aagagatgag	ccatctggtc	360
ctccagaggt	aaacaattta	caagagacac	atcaagccgg	c		401

<210> 34

<211> 401

<212> DNA

<213> Homo sapiens

<400> 34

tacgttagaa	ggaccctacg	ttagaaggg	gaggcgctag	ggccatagcc	taagggcact	60
gggaaccctg	tgggcatg	cagttcaagc	ccatccccgc	tccctccagc	tgtgtccat	120
cctgccaca	cctgaccatt	tgcctaacct	agatccttcc	tgtcttgcat	ttcctcaagc	180
atccggagcc	caggactgct	cagtcaacct	tctggaatgc	ccacaactcc	ccacaggcca	240
gccggccttg	ggactccgc	acagccacgt	gagccgggtg	agccgggtct	gtttgctagt	300
ggaggctgtt	aacagcacgg	gaagtggta	agggttcaac	aagagatgag	ccatctggtc	360
ctccagaggt	aaacaattta	caagagacac	atcaagccgg	c		401

<210> 35
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 35
 ggggtttcccc caagcccctt tccccctttg cgcctccac ttctcctaga ttgagagtca 60
 gcttggttct ttccctttaca tccattagtg agggtcaggc tcttttgta tgttttttt 120
 tcttttgat aacttaatta ttccagggtt cggggtgggc gctcgccct tgcccagtca 180
 cactggtgtg tgtgcgactc ctacaaagt aacagtttct ccagggtcaag ggggtgggatc 240
 caggcttggt gatgtgcaca atttcttttg tccacttgac acatctctgc gtctgattc 300
 tgctcaggga cggacccaag aacaaagcag ccatttaccg cctccggagg ggaggccagc 360
 cctgtggcac atccagggcc ttggaacacc tagagacaga t 401

<210> 36
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 36
 ggggtttcccc caagcccctt tccccctttg cgcctccac ttctcctaga ttgagagtca 60
 gcttggttct ttccctttaca tccattagtg agggtcaggc tcttttgta tgttttttt 120
 tcttttgat aacttaatta ttccagggtt cggggtgggc gctcgccct tgcccagtca 180
 cactggtgtg tgtgcgactc ttacaaagt aacagtttct ccagggtcaag ggggtgggatc 240
 caggcttggt gatgtgcaca atttcttttg tccacttgac acatctctgc gtctgattc 300
 tgctcaggga cggacccaag aacaaagcag ccatttaccg cctccggagg ggaggccagc 360
 cctgtggcac atccagggcc ttggaacacc tagagacaga t 401

<210> 37
 <211> 1068
 <212> PRT
 <213> Homo sapiens

<400> 37
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 Ile Arg Ser Gln Ser Phe Ala Gly Phe Ser Gly Leu Gln Glu Arg Arg
 20 25 30
 Ser Arg Cys Asn Ser Phe Ile Glu Asn Ser Ser Ala Leu Lys Lys Pro
 35 40 45
 Gln Ala Lys Leu Lys Lys Met His Asn Leu Gly His Lys Asn Asn Asn
 50 55 60
 Pro Pro Lys Glu Pro Gln Pro Lys Arg Val Glu Glu Val Tyr Arg Ala
 65 70 75 80
 Leu Lys Asn Gly Leu Asp Glu Tyr Leu Glu Val His Gln Thr Glu Leu
 85 90 95
 Asp Lys Leu Thr Ala Gln Leu Lys Asp Met Lys Arg Asn Ser Arg Leu
 100 105 110
 Gly Val Leu Tyr Asp Leu Asp Lys Gln Ile Lys Thr Ile Glu Arg Tyr
 115 120 125
 Met Arg Arg Leu Glu Phe His Ile Ser Lys Val Asp Glu Leu Tyr Glu
 130 135 140
 Ala Tyr Cys Ile Gln Arg Arg Leu Gln Asp Gly Ala Ser Lys Met Lys
 145 150 155 160
 Gln Ala Phe Ala Thr Ser Pro Ala Ser Lys Ala Ala Arg Glu Ser Leu
 165 170 175

Thr	Glu	Ile	Asn	Arg	Ser	Phe	Lys	Glu	Tyr	Thr	Glu	Asn	Met	Cys	Thr	
			180					185					190			
Ile	Glu	Val	Glu	Leu	Glu	Asn	Leu	Leu	Gly	Glu	Phe	Ser	Ile	Lys	Met	
		195					200					205				
Lys	Gly	Leu	Ala	Gly	Phe	Ala	Arg	Leu	Cys	Pro	Gly	Asp	Gln	Tyr	Glu	
	210				215						220					
Ile	Phe	Met	Lys	Tyr	Gly	Arg	Gln	Arg	Trp	Lys	Leu	Lys	Gly	Lys	Ile	
225				230					235						240	
Glu	Val	Asn	Gly	Lys	Gln	Ser	Trp	Asp	Gly	Glu	Glu	Thr	Val	Phe	Leu	
			245						250					255		
Pro	Leu	Ile	Val	Gly	Phe	Ile	Ser	Ile	Lys	Val	Thr	Glu	Leu	Lys	Gly	
		260						265					270			
Leu	Ala	Thr	His	Ile	Leu	Val	Gly	Ser	Val	Thr	Cys	Glu	Thr	Lys	Glu	
	275						280					285				
Leu	Phe	Ala	Ala	Arg	Pro	Gln	Val	Val	Ala	Val	Asp	Ile	Asn	Asp	Leu	
	290					295					300					
Gly	Thr	Ile	Lys	Leu	Asn	Leu	Glu	Ile	Thr	Trp	Tyr	Pro	Phe	Asp	Met	
305					310					315					320	
Glu	Asp	Met	Thr	Ala	Ser	Ser	Gly	Ala	Gly	Asn	Lys	Ala	Ala	Ala	Leu	
				325					330					335		
Gln	Arg	Arg	Met	Ser	Met	Tyr	Ser	Gln	Gly	Thr	Pro	Glu	Thr	Pro	Thr	
			340					345					350			
Phe	Lys	Asp	His	Ser	Phe	Phe	Arg	Trp	Leu	His	Pro	Ser	Pro	Asp	Lys	
	355						360					365				
Pro	Arg	Arg	Leu	Ser	Val	Leu	Ser	Ala	Leu	Gln	Asp	Thr	Phe	Phe	Ala	
	370					375					380					
Lys	Leu	His	Arg	Ser	Arg	Ser	Phe	Ser	Asp	Leu	Pro	Ser	Leu	Arg	Pro	
385				390					395						400	
Ser	Pro	Lys	Ala	Val	Leu	Glu	Leu	Tyr	Ser	Asn	Leu	Pro	Asp	Asp	Ile	
			405					410					415			
Phe	Glu	Asn	Gly	Lys	Ala	Ala	Glu	Glu	Lys	Met	Pro	Leu	Ser	Leu	Ser	
			420				425						430			
Phe	Ser	Asp	Leu	Pro	Asn	Gly	Asp	Cys	Ala	Leu	Thr	Ser	His	Ser	Thr	
	435					440						445				
Gly	Ser	Pro	Ser	Asn	Ser	Thr	Asn	Pro	Glu	Ile	Thr	Ile	Thr	Pro	Ala	
	450					455					460					
Glu	Phe	Asn	Leu	Ser	Ser	Leu	Ala	Ser	Gln	Asn	Glu	Gly	Met	Asp	Asp	
465				470					475					480		
Thr	Ser	Ser	Ala	Ser	Ser	Arg	Asn	Ser	Leu	Gly	Glu	Gly	Gln	Glu	Pro	
			485					490					495			
Lys	Ser	His	Leu	Lys	Glu	Glu	Asp	Pro	Glu	Glu	Pro	Arg	Lys	Pro	Ala	
			500					505					510			
Ser	Ala	Pro	Ser	Glu	Ala	Cys	Arg	Arg	Gln	Ser	Ser	Gly	Ala	Gly	Ala	
	515						520					525				
Glu	His	Leu	Phe	Leu	Glu	Asn	Asp	Val	Ala	Glu	Ala	Leu	Leu	Gln	Glu	
	530					535					540					
Ser	Glu	Glu	Ala	Ser	Glu	Leu	Lys	Pro	Val	Glu	Leu	Asp	Thr	Ser	Glu	
545				550					555					560		
Gly	Asn	Ile	Thr	Lys	Gln	Leu	Val	Lys	Arg	Leu	Thr	Ser	Ala	Glu	Val	
			565					570						575		
Pro	Met	Ala	Thr	Asp	Arg	Leu	Leu	Ser	Glu	Gly	Ser	Val	Gly	Gly	Glu	
	580							585					590			
Ser	Glu	Gly	Cys	Arg	Ser	Phe	Leu	Asp	Gly	Ser	Leu	Glu	Asp	Ala	Phe	
	595						600					605				
Asn	Gly	Leu	Leu	Leu	Ala	Leu	Glu	Pro	His	Lys	Glu	Gln	Tyr	Lys	Glu	
	610					615					620					
Phe	Gln	Asp	Leu	Asn	Gln	Glu	Val	Met	Asn	Leu	Asp	Asp	Ile	Leu	Lys	

625		630		635		640
Cys Lys Pro Ala Val Ser Arg Ser Arg Ser Ser Ser Leu Ser Leu Thr						
	645		650		655	
Val Glu Ser Ala Leu Glu Ser Phe Asp Phe Leu Asn Thr Ser Asp Phe						
	660		665		670	
Asp Glu Glu Glu Asp Gly Asp Glu Val Cys Asn Val Gly Gly Gly Ala						
	675		680		685	
Asp Ser Val Phe Ser Asp Thr Glu Thr Glu Lys His Ser Tyr Arg Ser						
	690		695		700	
Val His Pro Glu Ala Arg Gly His Leu Ser Glu Ala Leu Thr Glu Asp						
705		710		715		720
Thr Gly Val Gly Thr Ser Val Ala Gly Ser Pro Leu Pro Leu Thr Thr						
	725		730		735	
Gly Asn Glu Ser Leu Asp Ile Thr Ile Val Arg His Leu Gln Tyr Cys						
	740		745		750	
Thr Gln Leu Val Gln Gln Ile Val Phe Ser Ser Lys Thr Pro Phe Val						
	755		760		765	
Ala Arg Ser Leu Leu Glu Lys Leu Ser Arg Gln Ile Gln Val Met Glu						
	770		775		780	
Lys Leu Ala Ala Val Ser Asp Glu Asn Ile Gly Asn Ile Ser Ser Val						
785		790		795		800
Val Glu Ala Ile Pro Glu Phe His Lys Lys Leu Ser Leu Leu Ser Phe						
	805		810		815	
Trp Thr Lys Cys Ser Pro Val Gly Val Tyr His Ser Pro Ala Asp						
	820		825		830	
Arg Val Met Lys Gln Leu Glu Ala Ser Phe Ala Arg Thr Val Asn Lys						
	835		840		845	
Glu Tyr Pro Gly Leu Ala Asp Pro Val Phe Arg Thr Leu Val Ser Gln						
	850		855		860	
Ile Leu Asp Gln Ala Glu Pro Leu Leu Ser Ser Ser Leu Ser Ser Glu						
865		870		875		880
Val Val Thr Val Phe Gln Tyr Tyr Ser Tyr Phe Thr Ser His Gly Val						
	885		890		895	
Ser Asp Leu Glu Ser Tyr Leu Ser Gln Leu Ala Arg Gln Val Ser Met						
	900		905		910	
Val Gln Thr Leu Gln Ser Leu Arg Asp Glu Lys Leu Leu Gln Thr Met						
	915		920		925	
Ser Asp Leu Ala Pro Ser Asn Leu Leu Ala Gln Gln Glu Val Leu Arg						
	930		935		940	
Thr Leu Ala Leu Leu Leu Thr Arg Glu Asp Asn Glu Val Ser Glu Ala						
945		950		955		960
Val Thr Leu Tyr Leu Ala Ala Ala Ser Lys Asn Gln His Phe Arg Glu						
	965		970		975	
Lys Ala Leu Leu Tyr Tyr Cys Glu Ala Leu Thr Lys Thr Asn Leu Gln						
	980		985		990	
Leu Gln Lys Ala Ala Cys Leu Ala Leu Lys Ile Leu Glu Ala Thr Glu						
	995		1000		1005	
Ser Ile Lys Met Leu Val Thr Leu Cys Gln Ser Asp Thr Glu Glu Ile						
	1010		1015		1020	
Arg Asn Val Ala Ser Glu Thr Leu Leu Ser Leu Gly Glu Asp Gly Arg						
1025		1030		1035		1040
Leu Ala Tyr Glu Gln Leu Asp Lys Phe Pro Arg Asp Cys Val Lys Val						
	1045		1050		1055	
Gly Gly Arg His Gly Thr Glu Val Ala Thr Ala Phe						
	1060		1065			

<211> 591
 <212> PRT
 <213> Homo sapiens

<400> 38

Met	Leu	Val	Gly	Ser	Gln	Ser	Phe	Ser	Pro	Gly	Gly	Pro	Asn	Gly	Ile
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Ile	Arg	Ser	Gln	Ser	Phe	Ala	Gly	Phe	Ser	Gly	Leu	Gln	Glu	Arg	Arg
			20					25				30			
Ser	Arg	Cys	Asn	Ser	Phe	Ile	Glu	Asn	Ser	Ser	Ala	Leu	Lys	Lys	Pro
		35					40					45			
Gln	Ala	Lys	Leu	Lys	Lys	Met	His	Asn	Leu	Gly	His	Lys	Asn	Asn	Asn
	50					55				60					
Pro	Pro	Lys	Glu	Pro	Gln	Pro	Lys	Arg	Val	Glu	Glu	Val	Tyr	Arg	Ala
65					70				75					80	
Leu	Lys	Asn	Gly	Leu	Asp	Glu	Tyr	Leu	Glu	Val	His	Gln	Thr	Glu	Leu
			85					90					95		
Asp	Lys	Leu	Thr	Ala	Gln	Leu	Lys	Asp	Met	Lys	Arg	Asn	Ser	Arg	Leu
			100					105				110			
Gly	Val	Leu	Tyr	Asp	Leu	Asp	Lys	Gln	Ile	Lys	Thr	Ile	Glu	Arg	Tyr
	115					120						125			
Met	Arg	Arg	Leu	Glu	Phe	His	Ile	Ser	Lys	Val	Asp	Glu	Leu	Tyr	Glu
	130					135					140				
Ala	Tyr	Cys	Ile	Gln	Arg	Leu	Gln	Asp	Gly	Ala	Ser	Lys	Met	Lys	
145					150				155					160	
Gln	Ala	Phe	Ala	Thr	Ser	Pro	Ala	Ser	Lys	Ala	Ala	Arg	Glu	Ser	Leu
			165					170					175		
Thr	Glu	Ile	Asn	Arg	Ser	Phe	Lys	Glu	Tyr	Thr	Glu	Asn	Met	Cys	Thr
			180					185					190		
Ile	Glu	Val	Glu	Leu	Glu	Asn	Leu	Leu	Gly	Glu	Phe	Ser	Ile	Lys	Met
	195					200						205			
Lys	Gly	Leu	Ala	Gly	Phe	Ala	Arg	Leu	Cys	Pro	Gly	Asp	Gln	Tyr	Glu
	210					215					220				
Ile	Phe	Met	Lys	Tyr	Gly	Arg	Gln	Arg	Trp	Lys	Leu	Lys	Gly	Lys	Ile
225					230					235				240	
Glu	Val	Asn	Gly	Lys	Gln	Ser	Trp	Asp	Gly	Glu	Glu	Thr	Val	Phe	Leu
			245					250					255		
Pro	Leu	Ile	Val	Gly	Phe	Ile	Ser	Ile	Lys	Val	Thr	Glu	Leu	Lys	Gly
		260					265						270		
Leu	Ala	Thr	His	Ile	Leu	Val	Gly	Ser	Val	Thr	Cys	Glu	Thr	Lys	Glu
		275				280						285			
Leu	Phe	Ala	Ala	Arg	Pro	Gln	Val	Val	Ala	Val	Asp	Ile	Asn	Asp	Leu
	290					295					300				
Gly	Thr	Ile	Lys	Leu	Asn	Leu	Glu	Ile	Thr	Trp	Tyr	Pro	Phe	Asp	Met
305					310					315					320
Glu	Asp	Met	Thr	Ala	Ser	Ser	Gly	Ala	Gly	Asn	Lys	Ala	Ala	Ala	Leu
			325					330					335		
Gln	Arg	Arg	Met	Ser	Met	Tyr	Ser	Gln	Gly	Thr	Pro	Glu	Thr	Pro	Thr
			340					345					350		
Phe	Lys	Asp	His	Ser	Phe	Phe	Ser	Asn	Leu	Pro	Asp	Asp	Ile	Phe	Glu
		355					360					365			
Asn	Gly	Lys	Ala	Ala	Glu	Glu	Lys	Met	Pro	Leu	Ser	Leu	Ser	Phe	Ser
	370					375					380				
Asp	Leu	Pro	Asn	Gly	Asp	Cys	Ala	Leu	Thr	Ser	His	Ser	Thr	Gly	Ser
385					390					395					400
Pro	Ser	Asn	Ser	Thr	Asn	Pro	Glu	Ile	Thr	Ile	Thr	Pro	Ala	Glu	Phe
			405					410						415	

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Asn Leu Ser Ser Leu Ala Ser Gln Asn Glu Gly Met Asp Asp Thr Ser
      420                      425                      430
Ser Ala Ser Ser Arg Asn Ser Leu Gly Glu Gly Gln Glu Pro Lys Ser
      435                      440                      445
His Leu Lys Glu Glu Asp Pro Glu Glu Pro Arg Lys Pro Ala Ser Ala
      450                      455                      460
Pro Ser Glu Ala Cys Arg Arg Gln Ser Ser Gly Ala Gly Ala Glu His
      465                      470                      475                      480
Leu Phe Leu Glu Asn Asp Val Ala Glu Ala Leu Leu Gln Glu Ser Glu
      485                      490                      495
Glu Ala Ser Glu Leu Lys Pro Val Glu Leu Asp Thr Ser Glu Gly Asn
      500                      505                      510
Ile Thr Lys Gln Leu Val Lys Arg Leu Thr Ser Ala Glu Val Pro Met
      515                      520                      525
Ala Thr Asp Arg Leu Leu Ser Glu Gly Ser Val Gly Gly Glu Ser Glu
      530                      535                      540
Gly Cys Arg Ser Phe Leu Asp Gly Ser Leu Glu Asp Ala Phe Asn Gly
      545                      550                      555                      560
Leu Leu Leu Ala Leu Glu Pro His Lys Glu Gln Tyr Lys Glu Phe Gln
      565                      570                      575
Asp Leu Asn Gln Glu Val Met Asn Leu Asp Asp Ile Leu Lys Lys
      580                      585                      590

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<210> 39
<211> 1048
<212> PRT
<213> Homo sapiens

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<400> 39
Met Leu Val Gly Ser Gln Ser Phe Ser Pro Gly Gly Pro Asn Gly Ile
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Ile Arg Ser Gln Ser Phe Ala Gly Phe Ser Gly Leu Gln Glu Arg Arg
      20      25      30
Ser Arg Cys Asn Ser Phe Ile Glu Asn Ser Ser Ala Leu Lys Lys Pro
      35      40      45
Gln Ala Lys Leu Lys Lys Met His Asn Leu Gly His Lys Asn Asn Asn
      50      55      60
Pro Pro Lys Glu Pro Gln Pro Lys Arg Val Glu Glu Val Tyr Arg Ala
      65      70      75      80
Leu Lys Asn Gly Leu Asp Glu Tyr Leu Glu Val His Gln Thr Glu Leu
      85      90      95
Asp Lys Leu Thr Ala Gln Leu Lys Asp Met Lys Arg Asn Ser Arg Leu
      100     105     110
Gly Val Leu Tyr Asp Leu Asp Lys Gln Ile Lys Thr Ile Glu Arg Tyr
      115     120     125
Met Arg Arg Leu Glu Phe His Ile Ser Lys Val Asp Glu Leu Tyr Glu
      130     135     140
Ala Tyr Cys Ile Gln Arg Arg Leu Gln Asp Gly Ala Ser Lys Met Lys
      145     150     155     160
Gln Ala Phe Ala Thr Ser Pro Ala Ser Lys Ala Ala Arg Glu Ser Leu
      165     170     175
Thr Glu Ile Asn Arg Ser Phe Lys Glu Tyr Thr Glu Asn Met Cys Thr
      180     185     190
Ile Glu Val Glu Leu Glu Asn Leu Leu Gly Glu Phe Ser Ile Lys Met
      195     200     205
Lys Gly Leu Ala Gly Phe Ala Arg Leu Cys Pro Gly Asp Gln Tyr Glu
      210     215     220

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Ile	Phe	Met	Lys	Tyr	Gly	Arg	Gln	Arg	Trp	Lys	Leu	Lys	Gly	Lys	Ile
225					230					235					240
Glu	Val	Asn	Gly	Lys	Gln	Ser	Trp	Asp	Gly	Glu	Glu	Thr	Val	Phe	Leu
			245						250					255	
Pro	Leu	Ile	Val	Gly	Phe	Ile	Ser	Ile	Lys	Val	Thr	Glu	Leu	Lys	Gly
			260					265					270		
Leu	Ala	Thr	His	Ile	Leu	Val	Gly	Ser	Val	Thr	Cys	Glu	Thr	Lys	Glu
		275					280					285			
Leu	Phe	Ala	Ala	Arg	Pro	Gln	Val	Val	Ala	Val	Asp	Ile	Asn	Asp	Leu
290						295					300				
Gly	Thr	Ile	Lys	Leu	Asn	Leu	Glu	Ile	Thr	Trp	Tyr	Pro	Phe	Asp	Met
305					310					315					320
Glu	Asp	Met	Thr	Ala	Ser	Ser	Gly	Ala	Gly	Asn	Lys	Ala	Ala	Ala	Leu
				325					330					335	
Gln	Arg	Arg	Met	Ser	Met	Tyr	Ser	Gln	Gly	Thr	Pro	Glu	Thr	Pro	Thr
			340					345					350		
Phe	Lys	Asp	His	Ser	Phe	Phe	Arg	Trp	Leu	His	Pro	Ser	Pro	Asp	Lys
		355					360					365			
Pro	Arg	Arg	Leu	Ser	Val	Leu	Ser	Ala	Leu	Gln	Asp	Thr	Phe	Phe	Ala
370						375					380				
Lys	Leu	His	Arg	Ser	Arg	Ser	Phe	Ser	Asp	Leu	Pro	Ser	Leu	Arg	Pro
385					390					395					400
Ser	Pro	Lys	Ala	Val	Leu	Glu	Leu	Tyr	Ser	Asn	Leu	Pro	Asp	Asp	Ile
				405					410					415	
Phe	Glu	Asn	Gly	Lys	Ala	Ala	Glu	Glu	Lys	Met	Pro	Leu	Ser	Leu	Ser
			420					425					430		
Phe	Ser	Asp	Leu	Pro	Asn	Gly	Asp	Cys	Ala	Leu	Thr	Ser	His	Ser	Thr
		435					440					445			
Gly	Ser	Pro	Ser	Asn	Ser	Thr	Asn	Pro	Glu	Ile	Thr	Ile	Thr	Pro	Ala
450						455					460				
Glu	Phe	Asn	Leu	Ser	Ser	Leu	Ala	Ser	Gln	Asn	Glu	Gly	Met	Asp	Asp
465					470					475					480
Thr	Ser	Ser	Ala	Ser	Ser	Arg	Asn	Ser	Leu	Gly	Glu	Gly	Gln	Glu	Pro
				485					490					495	
Lys	Ser	His	Leu	Lys	Glu	Glu	Asp	Pro	Glu	Glu	Pro	Arg	Lys	Pro	Ala
			500					505					510		
Ser	Ala	Pro	Ser	Glu	Ala	Cys	Arg	Arg	Gln	Ser	Ser	Gly	Ala	Gly	Ala
		515					520					525			
Glu	His	Leu	Phe	Leu	Glu	Asn	Asp	Val	Ala	Glu	Ala	Leu	Leu	Gln	Glu
530						535					540				
Ser	Glu	Glu	Ala	Ser	Glu	Leu	Lys	Pro	Val	Glu	Leu	Asp	Thr	Ser	Glu
545					550					555					560
Gly	Asn	Ile	Thr	Lys	Gln	Leu	Val	Lys	Arg	Leu	Thr	Ser	Ala	Glu	Val
				565					570					575	
Pro	Met	Ala	Thr	Asp	Arg	Leu	Leu	Ser	Glu	Gly	Ser	Val	Gly	Gly	Glu
			580					585					590		
Ser	Glu	Gly	Cys	Arg	Ser	Phe	Leu	Asp	Gly	Ser	Leu	Glu	Asp	Ala	Phe
		595					600					605			
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625					630					635					640
Cys	Lys	Pro	Ala	Val	Ser	Arg	Ser	Arg	Ser	Ser	Ser	Leu	Ser	Leu	Thr
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Val	Glu	Ser	Ala	Leu	Glu	Ser	Phe	Asp	Phe	Leu	Asn	Thr	Ser	Asp	Phe
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Asp	Glu	Glu	Glu	Asp	Gly	Asp	Glu	Val	Cys	Asn	Val	Gly	Gly	Gly	Ala

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Asp	Ser	Val	Phe	Ser	Asp	Thr	Glu	Thr	Glu	Lys	His	Ser	Tyr	Arg	Ser
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Val	His	Pro	Glu	Ala	Arg	Gly	His	Leu	Ser	Glu	Ala	Leu	Thr	Glu	Asp
705					710					715					
Thr	Gly	Val	Gly	Thr	Ser	Val	Ala	Gly	Ser	Pro	Leu	Pro	Leu	Thr	Thr
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Thr	Gln	Leu	Val	Gln	Gln	Ile	Val	Phe	Ser	Ser	Lys	Thr	Pro	Phe	Val
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Ala	Arg	Ser	Leu	Leu	Glu	Lys	Leu	Ser	Arg	Gln	Ile	Gln	Val	Met	Glu
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Lys	Leu	Ala	Ala	Val	Ser	Asp	Glu	Asn	Ile	Gly	Asn	Ile	Ser	Ser	Val
785					790					795					
Val	Glu	Ala	Ile	Pro	Glu	Phe	His	Lys	Lys	Leu	Ser	Leu	Leu	Ser	Phe
805					810					815					
Trp	Thr	Lys	Cys	Cys	Ser	Pro	Val	Gly	Val	Tyr	His	Ser	Pro	Ala	Asp
820					825					830					
Arg	Val	Met	Lys	Gln	Leu	Glu	Ala	Ser	Phe	Ala	Arg	Thr	Val	Asn	Lys
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Glu	Tyr	Pro	Gly	Leu	Ala	Asp	Pro	Val	Phe	Arg	Thr	Leu	Val	Ser	Gln
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Ile	Leu	Asp	Gln	Ala	Glu	Pro	Leu	Leu	Ser	Ser	Ser	Leu	Ser	Ser	Glu
865					870					875					
Val	Val	Thr	Val	Phe	Gln	Tyr	Tyr	Ser	Tyr	Phe	Thr	Ser	His	Gly	Val
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Ser	Asp	Leu	Glu	Ser	Tyr	Leu	Ser	Gln	Leu	Ala	Arg	Gln	Val	Ser	Met
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Val	Gln	Thr	Leu	Gln	Ser	Leu	Arg	Asp	Glu	Lys	Leu	Leu	Gln	Thr	Met
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Thr	Leu	Ala	Leu	Leu	Leu	Thr	Arg	Glu	Asp	Asn	Glu	Val	Ser	Glu	Ala
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Leu	Gln	Lys	Ala	Ala	Cys	Leu	Ala	Leu	Lys	Ile	Leu	Glu	Ala	Thr	Glu
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Ser	Ile	Lys	Met	Leu	Val	Thr	Leu	Cys	Gln	Ser	Asp	Thr	Glu	Glu	Ile
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Gln	Ala	Lys	Leu	Lys	Lys	Met	His	Asn	Leu	Gly	His	Lys	Asn	Asn	Asn
	50					55					60				
Pro	Pro	Lys	Glu	Pro	Gln	Pro	Lys	Arg	Val	Glu	Glu	Val	Tyr	Arg	Ala
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Leu	Lys	Asn	Gly	Leu	Asp	Glu	Tyr	Leu	Glu	Val	His	Gln	Thr	Glu	Leu
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Asp	Lys	Leu	Thr	Ala	Gln	Leu	Lys	Asp	Met	Lys	Arg	Asn	Ser	Arg	Leu
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Gly	Val	Leu	Tyr	Asp	Leu	Asp	Lys	Gln	Ile	Lys	Thr	Ile	Glu	Arg	Tyr
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Met	Arg	Arg	Leu	Glu	Phe	His	Ile	Ser	Lys	Val	Asp	Glu	Leu	Tyr	Glu
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Ala	Tyr	Cys	Ile	Gln	Arg	Arg	Leu	Gln	Asp	Gly	Ala	Ser	Lys	Met	Lys
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Gln	Ala	Phe	Ala	Thr	Ser	Pro	Ala	Ser	Lys	Ala	Ala	Arg	Glu	Ser	Leu
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Thr	Glu	Ile	Asn	Arg	Ser	Phe	Lys	Glu	Tyr	Thr	Glu	Asn	Met	Cys	Thr
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Lys	Gly	Leu	Ala	Gly	Phe	Ala	Arg	Leu	Cys	Pro	Gly	Asp	Gln	Tyr	Glu
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Ile	Phe	Met	Lys	Tyr	Gly	Arg	Gln	Arg	Trp	Lys	Leu	Lys	Gly	Lys	Ile
225					230					235					240
Glu	Val	Asn	Gly	Lys	Gln	Ser	Trp	Asp	Gly	Glu	Glu	Thr	Val	Phe	Leu
				245					250					255	
Pro	Leu	Ile	Val	Gly	Phe	Ile	Ser	Ile	Lys	Val	Thr	Glu	Leu	Lys	Gly
			260					265					270		
Leu	Ala	Thr	His	Ile	Leu	Val	Gly	Ser	Val	Thr	Cys	Glu	Thr	Lys	Glu
		275					280					285			
Leu	Phe	Ala	Ala	Arg	Pro	Gln	Val	Val	Ala	Val	Asp	Ile	Asn	Asp	Leu
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Gly	Thr	Ile	Lys	Leu	Asn	Leu	Glu	Ile	Thr	Trp	Tyr	Pro	Phe	Asp	Met
305					310					315					320
Glu	Asp	Met	Thr	Ala	Ser	Ser	Gly	Ala	Gly	Asn	Lys	Ala	Ala	Ala	Leu
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Gln	Arg	Arg	Met	Ser	Met	Tyr	Ser	Gln	Gly	Thr	Pro	Glu	Thr	Pro	Thr
			340					345					350		
Phe	Lys	Asp	His	Ser	Phe	Phe	Ser	Asn	Leu	Pro	Asp	Asp	Ile	Phe	Glu
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Asn	Gly	Lys	Ala	Ala	Glu	Glu	Lys	Met	Pro	Leu	Ser	Leu	Ser	Phe	Ser
	370					375									